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13. ABSTRACT *(Maximum 200 words)*

The effects of cellular apoptotic regulators on tumor initiation and progression are difficult to predict, as oncogenes may have either anti-apoptotic (bcl-2) and pro-apoptotic (c-myc) effects. Anti-apoptotic genes may promote tumor growth by rescuing cells susceptible to apoptosis, due to DNA damage, for example. Pro-apoptotic genes, on the other hand, might increase DNA damage as a substrate for genetic instability. We tested the ability of transgenic bcl-2 to interact with DMBA in the formation of murine mammary tumors. A modest increase in tumor incidence at early time points (7-8 weeks post exposure) was observed in DMBA-treated transgenic vs control female mice. We have examined mammary tumors from transgenic mice for apoptosis using the in situ TUNEL assay. Unexpectedly, apoptotic cells were present at relatively high levels, compared to normal breast tissue (20.5 +/- 12.7/hpf vs 14.2 +/- 4.8/hpf).

Apoptosis is often associated with increased oxidative stress, a potential cause of DNA damage. We have examined Rat-1 cells undergoing c-myc-regulated cell death for early changes in mitochondrial structure and function . Induction of apoptosis led to initial mitochondrial proliferation followed by collapse of mitochondrial transmembrane potential . Increased numbers of mitochondria with a disorganized cristae and ultracondensed morphology were observed in myc-induced apoptosis. Constitutive c-myc expression has been demonstrated to lead to genetic instability. An association between mitochondrial dysfunction, ROS, and genetic instability may explain the apparent retention of apoptotic programs in experimental and human tumors.

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David Herbenick
Principal Investigator's Signature

5/12/98
Date

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Introduction

The bcl-2 gene is one of the best studied regulators of apoptosis, capable of inhibiting apoptotic cell deaths in a wide variety of experimental models (Hockenbery 1995). Several lines of evidence point to the importance of programmed cell death pathways as brakes against tumor development. The bcl-2 gene was first identified as an oncogene in follicular lymphomas bearing the t(14;18) chromosomal translocation. High bcl-2 expression in acute myelocytic leukemia correlates with poor chemotherapy responses and shortened survival (Campos and others 1993). Many studies implicate p53 function in apoptosis following gamma irradiation and exposure to certain chemotherapy drugs. Suppression of apoptosis during tumor growth is tightly linked to inhibition of p53 function and tumor progression in SV40 T antigen-induced choroid plexus tumors in transgenic mice, suggesting a wider role for p53 in apoptotic control (Symonds and others 1994).

Apoptotic mechanisms appear to be closely intertwined with other cellular processes, including cell division and differentiation (Rubin and others 1993), (Howard and others 1993). In support of this cross talk between pathways, overexpression of Bcl-2 has been shown to inhibit cell growth, promote G1-S cell cycle transition, or promote cellular differentiation in separate models (Pietenpol and others 1994), (Miyazaki and others 1995), (Linette and others 1994). Survival mediated by Bcl-2 in factor-deprived FDCPmix cells occurs with complete progression to differentiated

myeloid or erythroid phenotypes, while Bcl-xL maintains comparable survival of multipotent precursors. (Haughn and Hockenbery, unpublished data). The net effect of Bcl-2 overexpression in tumor cells is difficult to predict, in view of these multiple, sometimes opposing, effects. Although many tumors express high levels of Bcl-2, in breast cancers and an older age population with non-small cell lung cancers, Bcl-2 expression is correlated with a favorable prognosis (Joensuu and others 1994), (Leek and others 1994), (Bhargava and others 1994), (Pezzella and others 1993).

Paradoxically, several known oncogenes (c-fos, c-myc) are pro-apoptotic. Intermediate steps in transformation may be associated with lowered apoptotic thresholds (Preston and others, 1994). One possible explanation for these observations is that "apoptosis" contributes to full tumorigenicity in some way. While the phenotype of apoptotic death includes internucleosomal cleavage of DNA, whether sublethal activation of apoptotic pathways can occur is unknown. Infrequent double-stranded breaks may occur in this setting, which may increase the frequency of chromosomal rearrangements and amplifications, one form of genetic instability associated with tumors. The observation that Bcl-2 may inhibit apoptosis by increasing cellular resistance to oxidative stress is consistent with this hypothesis, as oxidative stress can be mutagenic and activate apoptotic cell death at different dose levels.

Based on experiments conducted in different systems, the anti-apoptotic effect of Bcl-2 could increase tumorigenesis, by sustaining cells that would be vulnerable to apoptosis at several steps in the tumorigenic process, or Bcl-2 could have a tumor suppressor effect, by inhibiting cell growth, promoting differentiation, or possibly by

counteracting a mechanism involved in genetic instability. While transgenic mice that express Bcl-2 in both B and T lymphocyte lineages are predisposed to cancer, the overall incidence of cancer is low and delayed when compared to other oncogenes. Other lineages that have been targeted for Bcl-2 overexpression in transgenic mice, including breast, intestine and myeloid, have not been noted to have an increased incidence of tumors (Lagasse and Weissman 1993), (Hockenbery, unpublished observations). Our goal is to determine the effect of bcl-2 overexpression in several tumor models and develop an understanding of how apoptosis interacts with the process of carcinogenesis, using breast cancer as our focus.

Body

Task 1 - Analysis of genetic instability in cell lines.

Cells triggered to undergo apoptosis have been found to have increased generation of reactive oxygen species. This change in redox state may be important in activation of caspase proteases, the executioners of apoptosis, as well as contribute to single-stranded DNA breaks observed in apoptosis (Nobel and others, 1997; Tschopp). The source of endogenous oxidative stress in apoptosis has been determined to be mitochondria, and the mechanisms of mitochondrial dysfunction in apoptosis remains an important problem in apoptosis research. Bcl-2 and other anti-apoptotic proteins are localized to mitochondrial membranes and prevent ROS generation as well as altered mitochondrial function during apoptosis. Bax, a pro-apoptotic factor also localized to mitochondria, results in rapid mitochondrial dysfunction characterized by initial hyperpolarization followed by eventual depolarization of mitochondria.

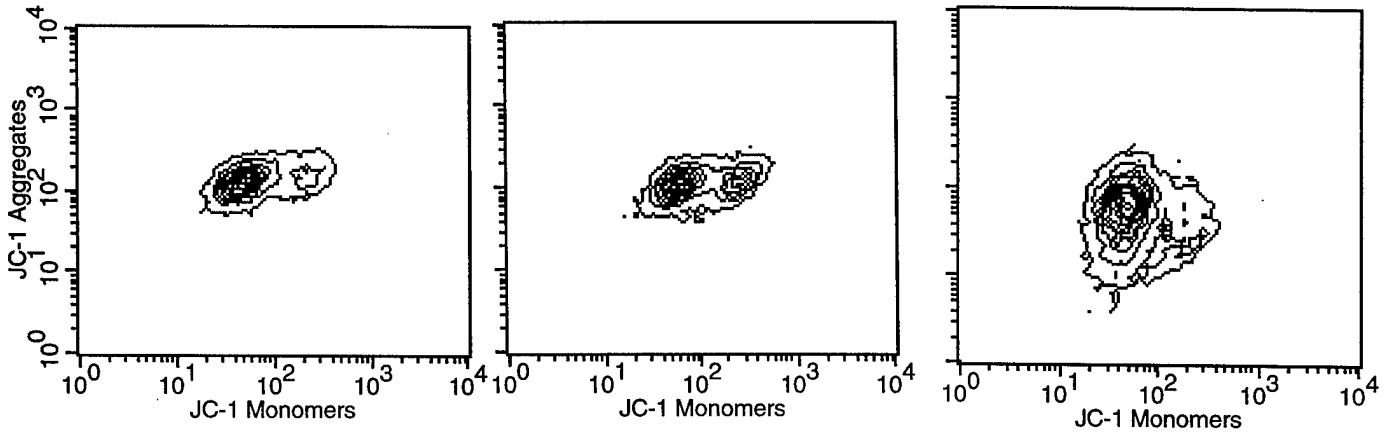
Rat-1 fibroblasts expressing the inducible myc-ER construct undergo myc-dependent apoptosis under low serum conditions. This model of apoptosis is also accompanied by increased ROS generation, as shown by the ROS-sensitive dye, dichlorofluorescein (DCFH). We characterized mitochondrial structure and function in Rat-1 cells according

to myc expression and serum conditions. 2 x 10^5 Rat-1 myc-ER cellswere plated in 10 cm dishes initially in phenol red-free DMEM with 10% FCS. After 1 day, cells were washed and switched to 0.1% FCS or recultured in 10% FCS. After an additional 2 days, myc induction was achieved by adding tamoxifen. Cells were tested for viability by trypan blue staining at sucessive time points. Mitochondrial staining with the fluorescent dye JC-1 was analyzed by flow cytometric measurement of FL-1 (green) and FL-2 (red) emissions. Specific staining of mitochondria by JC-1 includes a delta Ψm-independent component (green/monomers) and a delta Ψm-sensitive component (red/aggregates). Cells are harvested by trypsinization, incubated at 37° C with 1 μm JC-1 in culture media for 15 min, and analyzed using a Becton-Dickinson FACscan. At several time points, cell pellets were fixed in 1/2 strength Karnovsky's solution and processed for transmission electron microscopy.

Significant loss of viability only occured in tamoxifen-treated cells under low serum conditions. Cell death was first apparent at 48 hours after tamoxifen addition. Morphology of dead cells was consistent with apoptotic death. Rat-1 cells transfected with vector controls (pBabe-neo) retained high viability for all conditions. JC-1 staining was altered in tamoxifen-treated cells, but only in combination with low serum. The initial pattern of JC-1 staining consisted of an increase in green fluorescence seen at 24 hours (Figure 1). Subsequently, green^{HI} cells accumulated with low red staining. These

results suggested that mitochondria in myc-dependent apoptosis were initially triggered to proliferate and subsequently became depolarized.

Figure 1



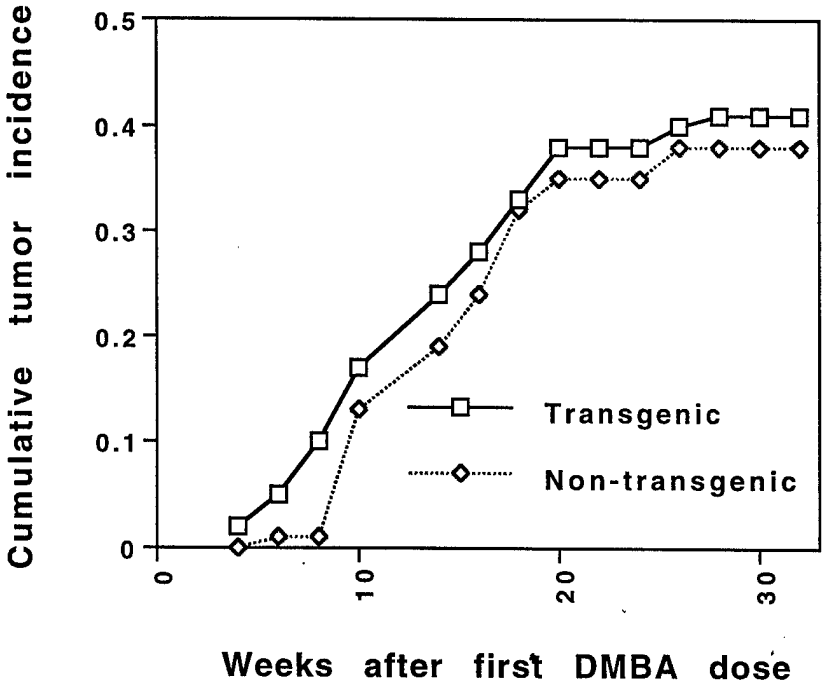
t0 **t24 hrs + tamoxifen** **t48 hrs + tamoxifen**

Electron micrographs demonstrated structural alterations corresponding to the JC-1 patterns. Serum-deprived, myc-induced cells contained greater numbers of mitochondria than under basal conditions. Mitochondrial structure was also altered, with elongated mitochondrial shapes and numerous, non-aligned cristae. The matrix space appeared dense, in some instances obscuring the pattern of cristae. The ultrastructural appearance of mitochondria in myc-induced, serum-starved cells suggested increased biogenesis of mitochondria and a pattern of mitochondrial injury previously described as ultra condensation. Bcl-2-protected cells appeared to have milder structural alterations, with an increase in cristae density.

Task 2 - Test of bcl-2 in murine mammary carcinogenesis models

A total of 72 transgenic MMTV-bcl-2 virgin female mice and 58 control littermates were treated with a total DMBA (dimethylbenzanthracene) dose of 6 mg and observed for the occurrence of mammary tumors. A small cooperative effect of bcl-2 on DMBA-induced mammary carcinogenesis was observed (Figure 2), however, an increase in tumor incidence/ week was only present at 7-8 weeks after the initiation of drug treatment.

Figure 2



As suppression of apoptosis was expected to be the mechanism of any interaction for bcl-2 with carcinogen exposure, we evaluated apoptosis within the mammary tumors for both genetic backgrounds. Mammary tumors were removed from mice at the time of

sacrifice, fixed in 10% neutral-buffered formalin and embedded in paraffin. Serial five-micron sections were processed by hematoxylin-eosin staining for tumor histology and TUNEL staining for apoptosis. Cells with TUNEL-positive nuclei were counted at high magnification from four random fields estimated to contain >80% tumor cells in a representative section from each tumor. Mammary tumors from control B6xC3H females had 14.2 +/- 4.8 apoptotic cells per high-power field (N = 7), while MMTV-bcl-2 transgenic-derived tumors had 20.5 +/- 12.7 apoptotic cells/hpf (N= 11). Transgenic mice were also noted to have non-uniform expression of the human Bcl-2 protein in mammary tumor sections, suggesting transgene down-regulation or silencing.

Our initial mating experience with MMTV-bcl-2 and myc mice resulted in few viable litters and we have had to set up additional mating pairs to obtain sufficient double transgenic females for analysis.

Task 3 - Analysis of the expression of genes regulating apoptosis during physiologic mammary epithelial cell death.

A cohort of virgin female FVB/N mice has been sacrificed with collection of mammary and vaginal tissues. Histologic staining of vaginal sections allows determination of the ovulatory cycle stage for paired mammary tissue blocks. Our initial examination of luteal phase mammary epithelium for Bcl-2, Bax, Bcl-x and Bak expression demonstrated

distinct patterns of expression for each protein. Bcl-2 is expressed in both ductal and lobular epithelium, although both regions are notably heterogenous. Bax is predominantly present in myoepithelial cells. Bcl-x has low expression with a fairly homogenous pattern. Finally, Bak is expressed principally in small terminal ductules.

Task 4 - Examination of hormonally treated and transgenic mice for apoptotic setpoints in mammary epithelium.

We have begun to collect mammary and vaginal tissue blocks from MMTV-myc and MMTV-bcl-2 females. Following the collection of these materials, we plan to initiate estrogen/progesterone treatment of cohorts using implanted osmotic pumps. We expect to be able to complete the analysis of these sections for apoptotic endpoints (TUNEL, Bcl-2 and related proteins) by the end of the year based on the assay throughput currently achievable in the lab.

Conclusions

The recent evidence that metastatic breast tumor DNA has both increased hydroxyl radical-induced damage as well as greater diversity of modified bases (Malins and others, 1996) is consistent with a role of oxidative stress in tumor progression. As Bcl-2 appears to modulate oxidative stress, probably via its interaction with mitochondrial functions, the relationship between the expression of Bcl-2 and related proteins and tumor progression may provide important insights into this process and its mechanisms. If tumor initiation and progression are related to suppression of apoptosis, the primary function of bcl-2, apoptotic indices should decrease in relation to tumor yield. Although synergy between Bcl-2 and carcinogen exposure was demonstrable, it was less than anticipated, based on oncogene interactions in cell and animal cancer models. Alternatively, Bcl-2 expression and apoptosis rates may reflect a selective pressure for an "oxidative" cellular redox state to increase DNA damage in cancer cells. In this model, the accumulation of apoptotic cells might represent the "tip of the iceberg" as the overt manifestation of more widespread cellular derangements causing sublethal genomic damage.

Our observations that changes in mitochondrial mass and function are associated with activation of an apoptotic pathway may provide an in situ method to monitor "apoptotic setpoints" and determine whether cells with low apoptotic setpoints are cancer-prone.

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